Supporting Information

Huang et al. 10.1073/pnas.1316622110



Fig. S1. (*A* and *B*) The mRNA (*A*) and protein (*B*) levels of ELONGATED HYPOCOTYL 5 (HY5) in response to photomorphogenic UV-B irradiation in Columbia (Col) seedlings grown under –UV-B for 4 d and then transferred to +UV-B for the indicated time. REGULATORY PARTICLE NON-ATPASE 6 (RPN6) is the loading control. (*C* and *D*) The effect of photomorphogenic UV-B on HY5 protein accumulation. Immunoblot analysis using 4-d-old alternative tandem affinity purification tag (TAPa-HY5)/*hy5-215* seedlings grown under –UV-B and +UV-B (*C*) or transferred from –UV-B to +UV-B for the indicated time (*D*).



Fig. S2. The mRNA levels of HY5 in Col seedlings grown under -UV-B or +UV-B for 4 d and then transferred to darkness for the indicated time.



Fig. S3. The protein levels of HY5 in 4-d-old –UV-B– and +UV-B–grown seedlings of Col, cop1-4 (A), cul4cs (B), uvr8-6 (C), and spa (D) mutants. (E) Immunoblot analysis of recombinant GST-HY5 in the cell-free degradation buffer without cell extracts at 22 °C for the indicated time.



Fig. S4. The mRNA levels of HY5 in 4-d-old –UV-B– and +UV-B–grown seedlings of YFP-UV RESISTANCE LOCUS 8 (UVR8)/uvr8-6, YFP-UVR8^{W285A}/uvr8-6, and YFP-UVR8^{W285F}/uvr8-6.

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Table S1. Summary of primers used in this study

PNAS PNAS

Assay	Construct	Primer ID	Primer sequence
Generation of transgenic plants	pF3PZPY122-UVR8	UVR8 5' Kpnl	ATACGGTACCATGGCGGAGGATATGGCT
	pJIM 19 (KAN)-FLAG-UVR8	UVR8 3' Xhol Sacl	ATACCTCGAGGAGCTCTCAAATTCGTACACGCTT
	pEarleyGate 104- <i>proUVR8</i> -YFP-	proUVR8 5' AfIII	ATACCTTAAGGTATATAGTACTTCCAATGGC
	UVR8	proUVR8 3' Aatll	ATACGACGTCATCACAGTTGCAGTTTTCACAAG
	pEarleyGate 104- <i>proUVR8</i> -YFP-UVR8 ^{W285A}	UVR8 W285A-F	TCTCCCAGATTTCGGGAGGTGCGAGACATACAATGGCATTGACTT
		UVR8 W285A-R	AAGTCAATGCCATTGTATGTCTCGCACCTCCCGAAATCTGGGAGA
	pEarleyGate 104-proUVR8-YFP-UVR8 ^{W285F}	UVR8 W285F-F	TCTCCCAGATTTCGGGAGGTTTTAGACATACAATGGCATTGACTT
		UVR8 W285F-R	AAGTCAATGCCATTGTATGTCTAAAACCTCCCGAAATCTGGGAGA
qRT-PCR		CHS-F	ACGTCACGTGTTGAGCGAGTATGG
		CHS-R	GAGGAACGCTGTGCAAGACGACTG
		At4g15480-F	AGTCGGGTTTATCGTTCT
		At4g15480-R	ATCCCTTTACCTTTAGCAC
		ELIP2-F	CACCACAAATGCCACAGTCT
		ELIP2-R	TGCTAGTCTCCCGTTGATCC
		HY5-F	TCAGAACGAGAACCAGATGCTTAG
		HY5-R	TTAGAACCACCACCACCTCCTC
Yeast three-hybrid	pGADT7-COP1 (no AD)	Y3H COP1 5' Kpnl	ATACGGTACCGCCATGGAAGAGATTTCGACGGA
		Y3H COP1 3' EcoRI	ATACGAATTCTCACGCAGCGAGTACCAGAACT

AD, activation domain; COP1, CONSTITUTIVE PHOTOMORPHOGENESIS 1.